

Sequence listing

<110> OncoMab GmbH

<120> Human monoclonal antibody

<150> EP - 03 026 161.4

<151> 2003-11-14

<160> 4

<210> 1

<211> 96

<212> DNA

<213> Homo sapiens

<220>

<223> Amino acid sequence of the variable region of the light chain (V_L) of antibody SAM-6

<400> 1

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Val | Leu | Thr | Gln | Pro | Pro | Ser | Val | Ser | Val | Ser | Pro | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Thr | Ala | Ser | Ile | Thr | Cys | Ser | Gly | Asp | Lys | Leu | Gly | Asp | Lys |
| | | | | 20 | | | | | 25 | | | | | 30 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Cys | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Val | Leu |
| | | | | 35 | | | | | 40 | | | | | 45 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Tyr | Gln | Asp | Ser | Lys | Arg | Pro | Ser | Gly | Ile | Pro | Glu | Arg |
| | | | | 50 | | | | | 55 | | | | | 60 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Gly | Ser | Asn | Ser | Gly | Asn | Thr | Ala | Thr | Leu | Thr | Ile | Ser |
| | | | | 65 | | | | | 70 | | | | | 75 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Gln | Ala | Met | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Gln | Ala | Trp |
| | | | | 80 | | | | | 85 | | | | | 90 |

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Ser | Ile | Val | Val |
| | | | | 95 | |

<210> 2

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotide sequence of the variable region of the light chain (V_L) of antibody SAM-6

<400> 2

| | |
|---|-----|
| tcc tat gtg ctg act cag cca ccc tca gtg tcc gtg tcc cca gga | 45 |
| Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly | |
| 1 5 10 15 | |
| CDR1 | |
| cag aca gcc agc atc acc tgc tct gga gat aaa ttg ggg gat aaa | 90 |
| Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys | |
| 20 25 30 | |
| CDR2 | |
| tat gct tgc tgg tat cag cag aag cca gcc cag tcc cct gtg ctg | 135 |
| Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu | |
| 35 40 45 | |
| CDR2 | |
| gtc atc tat caa gat agc aag cgg ccc tca ggg atc cct gag cga | 180 |
| Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg | |
| 50 55 60 | |
| ttc tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc | 225 |
| Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser | |
| 65 70 75 | |
| ggg acc cag gct atg gat gag gct gac tat tac tgt cag gcg tgg | 270 |
| Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp | |
| 80 85 90 | |
| CDR3 | |
| gac agc agc att gtg gta | 288 |
| Asp Ser Ser Ile Val Val | |
| 95 | |

<210> 3

<211> 110

<212> DNA

<213> Homo sapiens

<220>

<223> Amino acid sequence of the variable region of the heavy chain (V_H) of antibody SAM-6

<400> 3

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

Lys Thr Phe Asp Tyr
110

$\langle 210 \rangle_4$

$\langle 211 \rangle$ 330

<212> DNA

◁213>.Homo sapiens

<220>

<223> Nucleotide sequence of the variable region of the heavy chain (V_H) of antibody SAM-6

<400> 4

cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg 45
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 90
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

CDR1

agc tat gct atg cac tgg gtc cgc cag gct cca gcc aag ggg ctg 135
Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu
 35 40 45

CDR2

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac 180
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc 225
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag gac 270
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

CDR3

acg gct gtg tat tac tgt gcg aga gat cgg tta gca gtg gct ggt 315
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

aaa act ttt gac tac
Lys Thr Phe Asp Tyr
110